

Application No.: 10/632,099
Reply to Final Office Action dated July 2, 2010
Response Final Office Action filed on November 2, 2010

SUMMARY OF CLAIMS

Claims 1 and 3-5 have been amended. Claims 2, 6, 7, 10-12 and 15-61 are cancelled. Claims 1, 3-5, 8, 9, 13, 14 and 62-78 are currently pending and under consideration.

REMARKS

Claims 1-5, 7-9, 13, 14 and 62-78 are rejected under 35 U.S.C. 103(a) as being unpatentable over Hughes et al. (Cell, 2000, 102, 109-126) in view of Meltzer (Current Opinion in Genetics & Development, 2001, 11, 258-263) and further in view of Cho et al. (US 6,741,986). Applicants respectfully traverse this rejection, but in the interest of expediting prosecution have amended the claims. Specifically claim 1 now recites the limitations of dependant claims 2 and 7, which individually have been canceled. Reconsideration and allowance of the application are requested in view of the current claims and the following attorney argument.

I. Meltzer fails to disclose the ontology recited in the present claims.

Applicant submits that the Office can not establish a *prima facie* case of obviousness against the currently amended claims based upon the Hughes, Meltzer, and Cho references. Taken together, these three references do not alone or in any combination teach or suggest all elements of the current claim 1. Accordingly, Applicants respectfully request withdrawal of this rejection.

Current claim 1 requires that the ontology is organized so that: (i) each gene, mRNA, protein expressed from said gene, and biological effect is given an identifier which is related to synonyms for the identifier; (ii) each gene, mRNA, protein expressed from said gene, and biological effect is categorized by class; and (iii) the relationship of each gene, mRNA, protein expressed from said gene and disease state is defined by slots and facets. This ontology is not described in any disclosed reference.

The Examiner argues that “Meltzer teaches a gene *ontology* database and a *system*, i.e. high-density array pattern interpreter, where search engines carry out computations with the output of

expression databases (page 260, right column, second and third paragraphs)” (Office Action of 7/2/10 page 4 emphasis added).

Regarding the Meltzer “ontology” (Meltzer page 260 column 2, 1st full paragraph), Meltzer does not describe how the ontology is organized beyond merely stating that “genes are categorized in three hierarchical schemes according to molecular function, biological process and cellular component.” This disclosure fails to teach or suggest the ontology of the present claims. With the limited disclosure in Meltzer, one skilled in the art would not have been able to begin with the Hughes disclosure and combine the teachings of Meltzer to arrive at the present claims. Cho does not correct this deficiency.

Regarding the Meltzer “system” (Meltzer page 260 column 2, 2nd full paragraph), Meltzer states that the systems are “*under development*” and it is “*anticipated* that search engines can carry out these computations” (emphasis added). Thus, after reading Meltzer one skilled in the art would infer that such a system was not yet in existence. Furthermore, there is no indication that the Meltzer “system” is even organized as an ontology. As such, one skilled in the art would not have been able to modify the Hughes disclosure and combine Meltzer to arrive at the present claims. Again, Cho does not correct this deficiency.

It should also be noted that Meltzer states that “[i]n contrast to clustering samples and genes, *the interpretation of expression data to infer the pathways affected by a disease gene mutation is much more problematic*” (Meltzer page 260 column 1, 5th full paragraph, emphasis added). Meltzer later goes on to state that “[i]ntensive efforts to establish alternate computational methods [to extract functionally related genes] *are continuing*” (Meltzer page 260 column 2, 3rd full paragraph, emphasis added). These statements highlight the difficulty one skilled in the art faced at the time Meltzer was published and that solutions to these problems were not known at the time.

II. The proposed modification would render Hughes useless.

Hughes discloses a compendium consisting of 300 full-genome expression profiles in *S. cerevisiae*. The expression profiles in the compendium are reference profiles, generated by exposing the *S. cerevisiae* to various known agents under controlled conditions. The Hughes method then

involves generating a new full-genome expression profile after exposing an *S. cerevisiae* to an experimental agent under similar controlled conditions. Inferences about the experimental agent are made based upon which profiles in the compendium the new profile most closely matches after a statistical analysis.

As stated in Hughes, “[a]ll experiments were conducted under single growth condition, allowing the direct comparison of all genes over all profiles” (Hughes page 111, 1st full paragraph). The fact that all the data in the compendium is derived under the same conditions give statistical power to the comparison. Altering Hughes by adding data not generated using similar growth conditions, for instance by extracting data from a combination of proprietary and public data sources, would hinder the main advantages of the technique. Additionally, the addition of outside data would also make the data from the series of 63 negative control experiments less useful (Hughes pages 111-112).

Furthermore, organizing the dataset from Hughes as an ontology does not add any statistical or computational power to the technique. In Hughes, because the data come from similar sources there is no need to organize the data as an ontology. The expression profiles are all the same kind of data, set for a direct comparison. Reorganization of the data into an Ontology would make the Hughes technique more complicated for no gain and may make the technique statistically less powerful.

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CONCLUSION

Applicants submit that this paper fully addresses the Office Action mailed July 2, 2010. Should the Examiner have any question, the Examiner is encouraged to telephone the undersigned. The Commissioner is authorized to charge any underpayment or credit any overpayment to Deposit account No. 23-2415 (Attorney Docket No.: 27763-705.501) for any matter in connection with this response, including any fee for extension of time, which may be required.

Respectfully submitted,

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